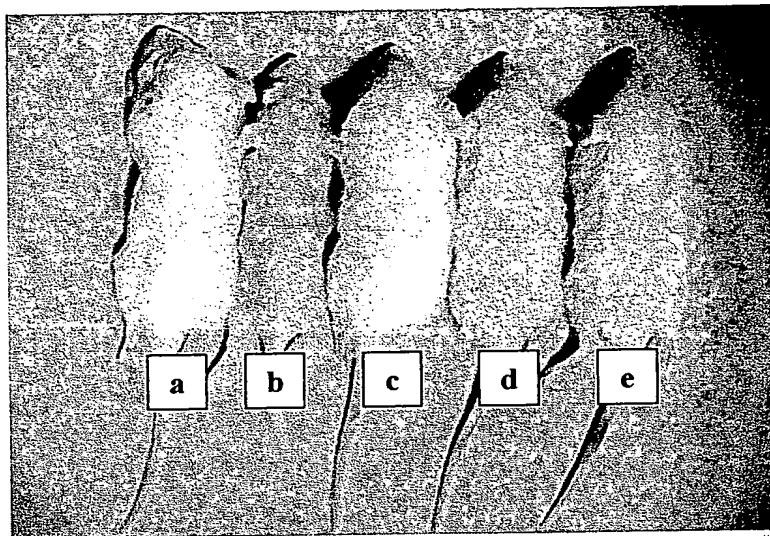


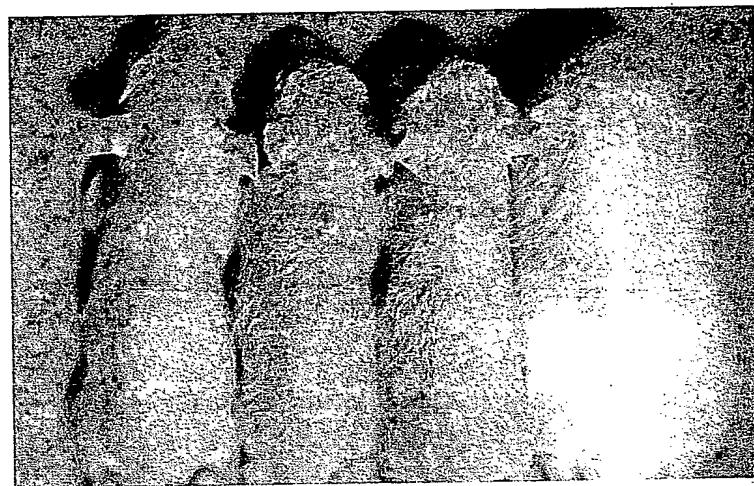
FIGURE 1



- a** untreated control
- b** Ara-c control
- c** SEQ ID NO: 2
- d** SEQ ID NO: 3
- e** SEQ ID NO: 22

1000 2000 3000 4000 5000 6000 7000 8000 9000 10000

FIGURE 2



Ara-c control

0.1mg

Ara-c +SEQ ID NO: 10

0.5mg

$2.5mg$

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FIGURE 3A

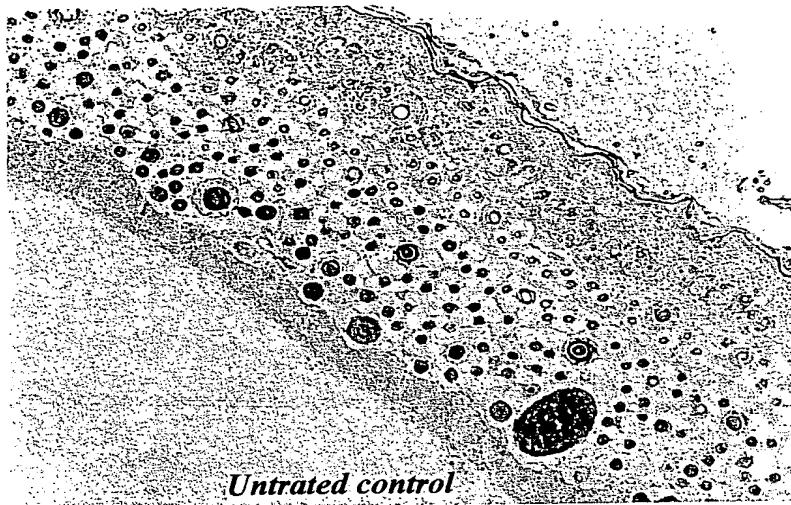


FIGURE 3B

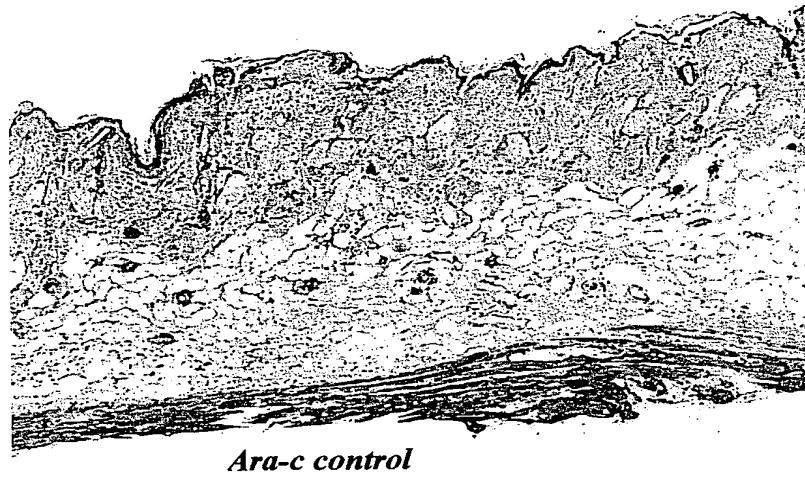
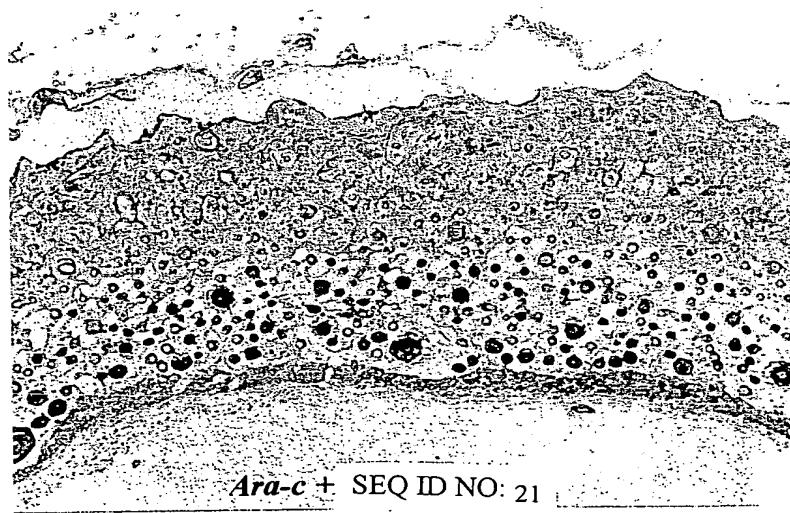


FIGURE 3C



4 0 0 3 2 3 0 0 1 1 2 3 1 0 1

FIGURE 4

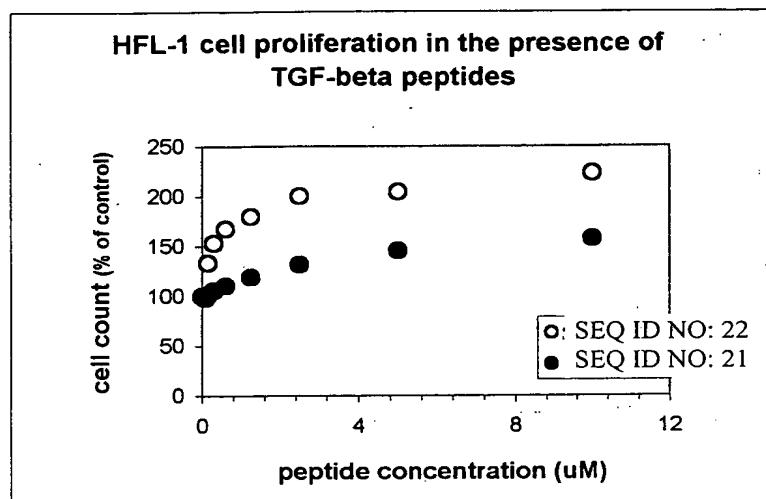


FIGURE 5A

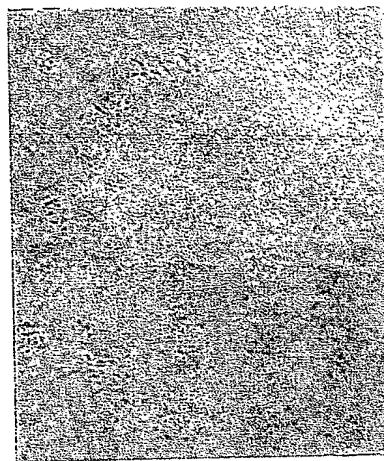


FIGURE 5B

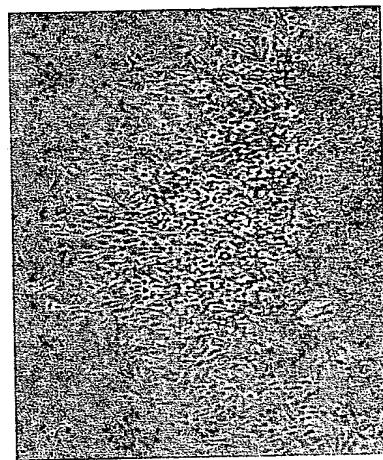


FIGURE 5C



FIGURE 5D

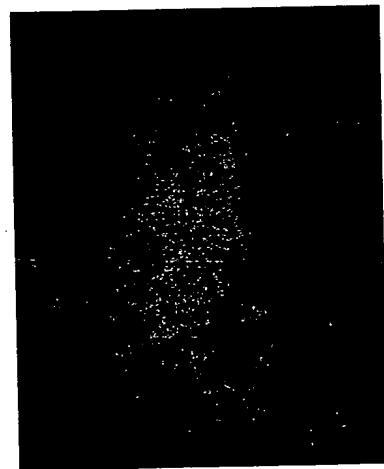


FIGURE 6A

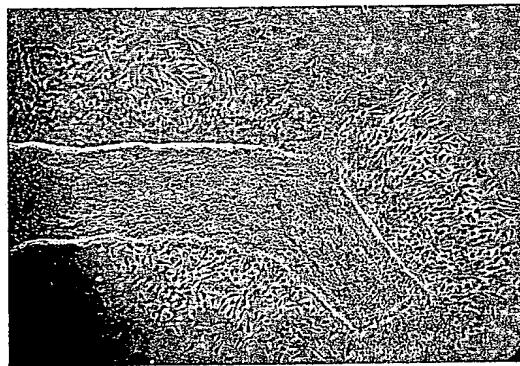


FIGURE 6B

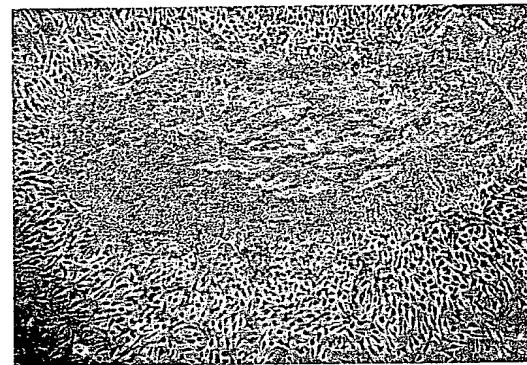


FIGURE 6C

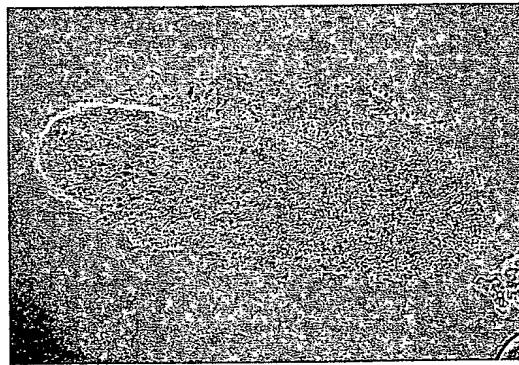


FIGURE 6D

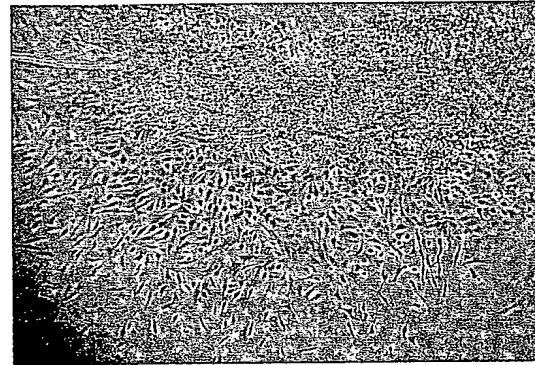


FIGURE 7

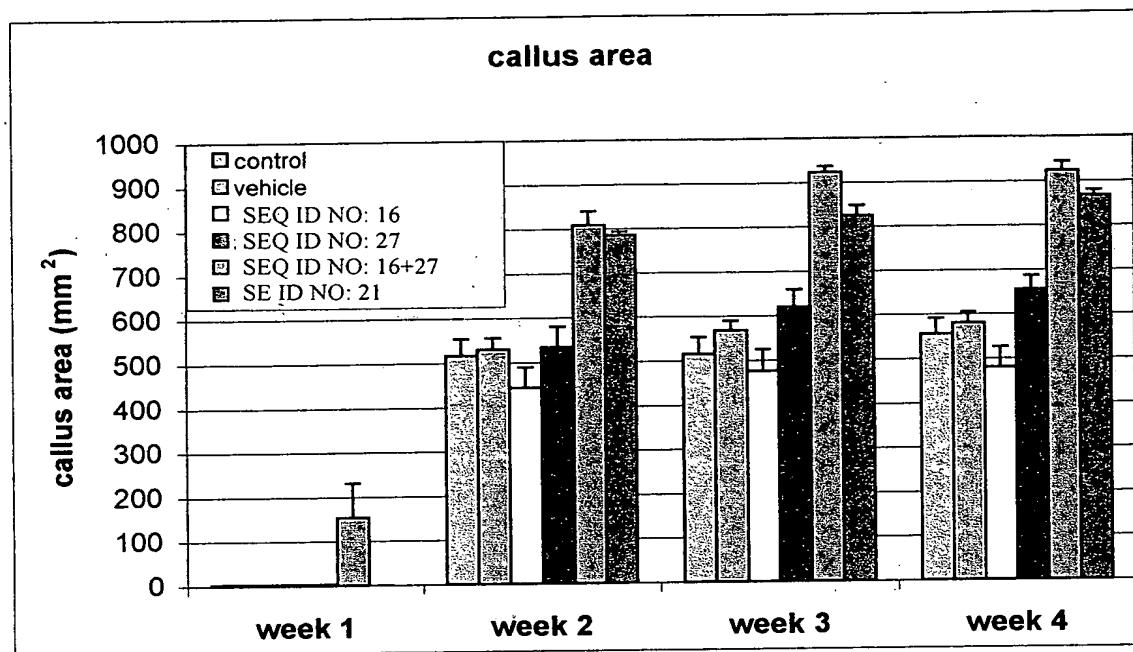


FIGURE 8

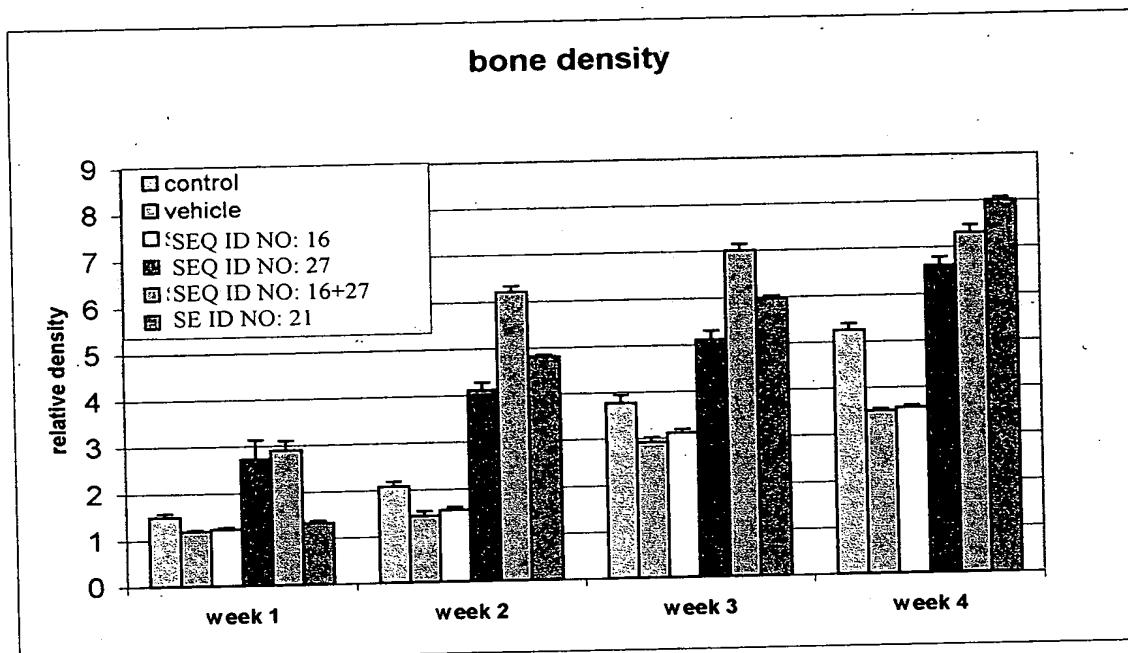


FIGURE 9

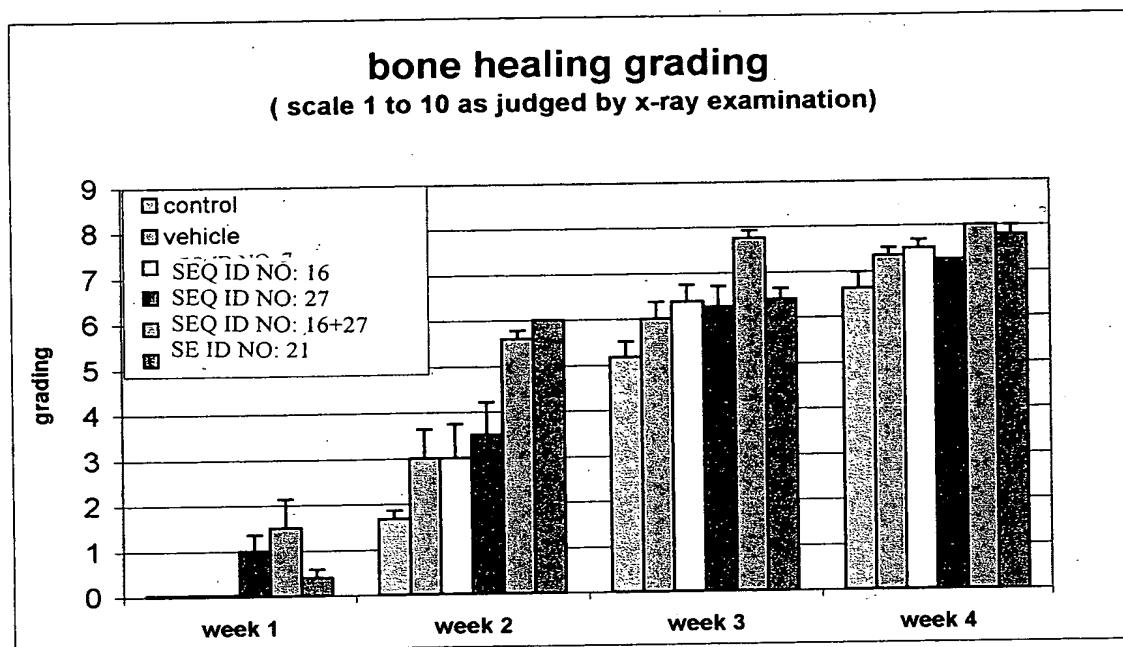


FIGURE 10A

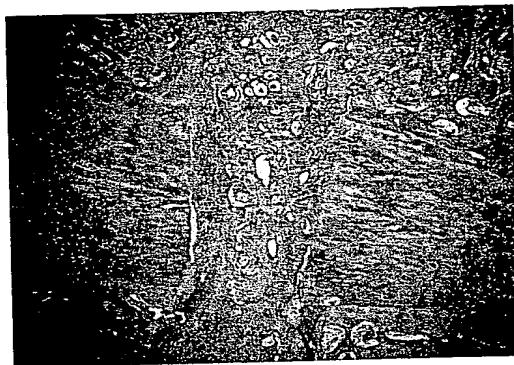


FIGURE 10B



FIGURE 11A



FIGURE 11B

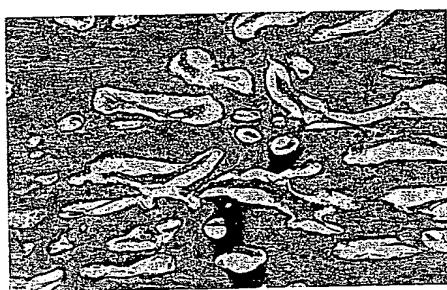


Fig 12

HJ-loop

TBR1	EIARRCSIGGI---HEDYQLPYYDLVPSDPSVEE
ACTR2	ELVSRCKAADG--PVDEYMLPFEETIGQHPSLEE
BMR2	EIFMRCTDLFPGESVPEYQMAFQTEVGNHPTFED
TBR2	EMTSRCNAVGE---VKDYEPFGSKVREHPCVES
ALK4	EIARRCNSGGV---HEEYQLPYYDLVPSDPSIEE
ALK3	EMARRCITGGI---VEEYQLPYYNMVPSPSYED
ALK1	EIARRTIVNGI---VEDYRPPFYDVVPNDPSFED
	*: * : * .. : .. * *.

Alpha-D region

CLUSTAL X (1.81) multiple sequence alignment

TBR1	----SDYHEHGSFLFDYLNRYTVTVE
ACTR2	----TAFHDKGSLTDYLKGNIITWNE
BMR2	----MEYYPNGLCKYLSLHTSDWV
TBR2	TAFHAKGNLQEYLTRHVISWE
ALK4	----SDYHEHGSFLFDYLNRYTVTIE
ALK3	----TDYHENGSLYDFLKCATLDTR
ALK1	----THYHEHGSLYDFLQRQTLERPH
	: : : * . : *

B4-B5 region

TBR1	ADNKDNG-TWTQLWLVS
ACTR2	AEKRGSS-LEAELWLITA
BMR2	GDERVTADGRMEYLLVME
TBR2	AEERKTE-LGKQYWLITA
ALK4	ADNKDNG-TWTQLWLVS
ALK3	ADIKGTG-SWTQLYLITD
ALK1	SDMTSRN-SSTQLWLITH
	: : : * :

A-region

TBR1	----QTVMLRHENILGFIA
ACTR2	----STPGMKHENLLQFIA
BMR2	----RVPLMEHDNIARFIV
TBR2	SDINLKHENILQFLT
ALK4	----QTVMLRHENILGFIA
ALK3	----QTVMLRHENILGFIA
ALK1	----NTVLLRHNDNILGFIA
	: : * : * : * : .